

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2004, 19:35:16 ; Search time 21.9375 Seconds  
(without alignments)  
39.474 Million cell updates/sec

Title: US-10-618-644-4

Perfect score: 58

Sequence: 1 IPPGVPTWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.4

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	212	2 JA0152	glycinin chain A7
2	58	100.0	560	2 S11004	glycinin G4 precu
3	58	100.0	562	2 S20946	glycinin Gv4 precu
4	58	100.0	563	2 S54802	glycinin A5A4B3 ch
5	57	98.3	136	2 T12140	legumin - fava bea
6	57	98.3	564	2 S37241	legumin B - fava b
7	57	98.3	566	2 T06453	probable legumin B
8	52	89.7	562	1 FWSYG5	glycinin chain A5A
9	49	84.5	290	2 JC2097	legumin type B alp
10	49	84.5	484	2 A24942	legumin B4 precu
11	49	84.5	485	2 S44268	legumin B precu
12	49	84.5	500	2 S26688	legumin K - garden
13	49	84.5	503	2 S00336	legumin B LegJ pre
14	48	82.8	516	1 FWSYG3	glycinin G5 precu
15	43	74.1	168	2 T40893	hypothetical prote
16	42	72.4	503	2 E72078	probable sodium-tr
17	42	72.4	503	2 A86544	NADH (ubiquinone)
18	42	72.4	503	2 B81690	probable sodium-tr
19	42	72.4	503	2 C71535	probable NADH (ubi
20	42	72.4	705	2 S51635	fibroblast growth
21	42	72.4	707	2 A38429	keratinocyte growt
22	41	70.7	180	2 F72722	hypothetical prote
23	41	70.7	299	2 D95382	probable transcrip
24	41	70.7	379	2 T37274	probable cathepsin
25	41	70.7	2338	2 T25810	probable cathepsin
26	40	69.0	156	2 AG0243	probable exported
27	40	69.0	311	2 AB1880	hypothetical prote
28	40	69.0	353	2 AF0676	hydrogenase-1 oper
29	40	69.0	358	2 F64136	rnfD protein homol

30 39.5 68.1 454 2 T36209 probable pyridine  
31 39 67.2 235 2 A22962 carbonate dehydrat  
32 39 67.2 329 2 S07577 legumin storage pr  
33 39 67.2 335 2 S07578 legumin storage pr  
34 39 67.2 335 2 S07576 legumin storage pr  
35 39 67.2 382 2 AF2460 glycosyltransferas  
36 39 67.2 433 2 S51767 glycosyl transfera  
37 39 67.2 502 2 A55197 Wiskott-Aldrich sy  
38 39 67.2 591 2 H83362 gluconate dehydrog  
39 39 67.2 731 2 D90483 alpha-xylosidase (  
40 39 67.2 783 2 T35389 probable serine-th  
41 39 67.2 1067 2 D82436 transporter, AcRB/  
42 39 67.2 1095 2 T01916 hypothetical prote  
43 39 67.2 1174 2 T08196 hypothetical prote  
44 39 67.2 2105 2 T18968 probable serine-ty  
45 39 67.2 2896 2 T30939 hemocyanin G-type

#### ALIGNMENTS

##### RESULT 1

JA0152

glycinin chain A7 - soybean

N;Alternate names: seed storage protein

C;Species: Glycine max (soybean)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 24-Feb-1995

C;Accession: JA0152

R;Kagawa, H.; Hirano, H.

Plant Sci. 56, 189-195, 1988

A;Title: Identification and structural characterization of the glycinin seed storage pr.

A;Reference number: JA0152

A;Accession: JA0152

A;Molecule type: protein

A;Residues: 1-212 <KAG>

A;Experimental source: seed

C;Comment: Glycinin is the most abundant protein in the soybean seeds. A7 chain is one

C;Superfamily: glycinin

Query Match 100.0%; Score 58; DB 2; Length 212;

Best Local Similarity 100.0%; Pred. No. 0.047; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPPGVPTWT 9

Db 29 IPPGVPTWT 37

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

QY 1 IPPGVPEYWT 9  
|||||  
Db 149 IPPGVPEYWT 157

## RESULT 3

S20946  
glycinin Gy4 precursor - soybean (cv. Forrest)  
C:Species: Glycine max (soybean)  
A:Variety: cv. Forrest  
C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
R:Xue, Z.T.; Xu, M.L.; Shen, W.; Zhuang, N.L.; Hu, W.M.; Shen, S.C.  
Plant Mol. Biol. 18, 897-908, 1992  
A:Title: Characterization of a Gy4 glycinin gene from soybean Glycine max cv. Forrest.  
A:Reference number: S20946; MUID:92256811; PMID:1316192  
A:Accession: S20946  
A:Molecule type: DNA  
A:Residues: 1-562 <XUE>  
A:Cross-references: UNIPROT:Q43452; EMBL:X52863; NID:g18640; PIDN:CAA37044.1; PID:g18641  
A:Experimental source: cv. Forrest  
C:Genetics:  
A:Gene: Gy4  
A:Introns: 97/1; 184/3; 433/3  
C:Superfamily: glycinin  
C:Keywords: seed; storage protein  
F:1-23/Domatin: signal sequence #status predicted <SIG>  
F:24-562/Product: glycinin Gy4 #status predicted <MAT>

Query Match 100.0%; Score 58; DB 2; Length 562;  
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 IPPGVPEYWT 9  
|||||  
Db 148 IPPGVPEYWT 156

## RESULT 4

S54802  
glycinin A5A4B3 chain - soybean  
C:Species: Glycine max (soybean)  
C:Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S54802  
R:Xue, Z.  
submitted to the EMBL Data Library, May 1995  
A:Reference number: S54802  
A:Accession: S54802  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-563 <XUE>  
A:Cross-references: UNIPROT:Q39921; EMBL:X86970; NID:g806555; PIDN:CAA60533.1; PID:g8065  
C:Superfamily: glycinin

Query Match 100.0%; Score 58; DB 2; Length 563;  
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 IPPGVPEYWT 9  
|||||  
Db 149 IPPGVPEYWT 157

## RESULT 5

T12140  
legumin - fava bean (fragment)  
C:Species: Vicia faba (fava bean)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T12140  
R:Heim, U.; Baeumlein, H.; Wobus, U.  
Plant Mol. Biol. 25, 131-135, 1994  
A:Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a hig

A:Reference number: S46503; MUID:94272010; PMID:8003694  
A:Accession: T12140  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-136 <HEI>  
A:Cross-references: UNIPROT:Q43672; EMBL:Z26487; NID:g403333; PIDN:CAA81261.1; PID:g4033  
C:Genetics:  
A:Gene: LelB161  
A:Note: intron positions not resolved (incomplete sequence)  
C:Superfamily: glycinin  
C:Keywords: seed; storage protein

Query Match 98.3%; Score 57; DB 2; Length 136;  
Best Local Similarity 88.9%; Pred. No. 0.042; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

QY 1 IPPGVPEYWT 9  
|||||  
Db 50 IPPGVPEYWT 58

## RESULT 6

S37241  
legumin B - fava bean  
C:Species: Vicia faba (fava bean)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S46503; S37241  
R:Heim, U.; Baeumlein, H.; Wobus, U.  
Plant Mol. Biol. 25, 131-135, 1994  
A:Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a hig  
A:Reference number: S46503; MUID:94272010; PMID:8003694  
A:Accession: S46503  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-564 <HE2>  
A:Cross-references: UNIPROT:Q43673; EMBL:Z26489; NID:g403335; PIDN:CAA81262.1; PID:g4033  
C:Genetics:  
A:Introns: 178/3; 439/3  
C:Superfamily: glycinin

Query Match 98.3%; Score 57; DB 2; Length 564;  
Best Local Similarity 88.9%; Pred. No. 0.19; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

QY 1 IPPGVPEYWT 9  
|||||  
Db 142 IPPGVPEYWT 150

## RESULT 7

T06453  
probable legumin B - garden pea  
C:Species: Pisum sativum (garden pea)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06453  
R:Brown, D.P.  
submitted to the EMBL Data Library, June 1992  
A:Reference number: Z15688  
A:Accession: T06453  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-566 <BOW>  
A:Cross-references: UNIPROT:Q24294; EMBL:X67424; PIDN:CAA47809.1  
A:Experimental source: cv. Feltham First  
C:Genetics:  
A:Gene: legs  
C:Superfamily: glycinin  
C:Keywords: seed; storage protein

Query Match 98.3%; Score 57; DB 2; Length 566;  
Best Local Similarity 88.9%; Pred. No. 0.19; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 1; Mismatches 1;

QY 1 IPPGVPT 9  
|||:||||  
Db 144 IPPGIPYT 152

RESULT 8  
FWSYG5  
glycinin chain A5A4B3 precursor - soybean  
N;Alternate names: 11S globulin  
C;Species: Glycine max (soybean)  
C;Date: 28-Feb-1986 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A91145; A91333; A03348; A25207; A27253  
R;Momma, T.; Negro, T.; Hirano, H.; Matsumoto, A.; Uda, K.; Fukazawa, C.  
Eur. J. Biochem. 149, 491-496, 1985  
A;Title: Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a splitting site  
A;Reference number: A91145; MUID:85230642; PMID:2988947  
A;Accession: A91145  
A;Molecule type: mRNA  
A;Residues: 1-562 <WOM>  
A;Cross-references: UNIPROT:P02858; GB:X02626; NID:G18628; PIDN:CAA26478.1; PID:G732706  
A;Experimental source: cv. Bonminor  
A;Note: the authors translated the codon TCA for residue 86 as Leu, GAC for residue 145  
R;Hirano, H.; Fukazawa, C.; Harada, K.  
FEBS Lett. 181, 124-128, 1985  
A;Title: The primary structures of the A4 and A5 subunits are highly homologous to that  
A;Reference number: A91333  
A;Accession: A91333  
A;Molecule type: protein  
A;Residues: 24-28, 'F', '30-81', 'L', '83-85', 'L', '87-93', 'V', '95-100', 'I', '102', 'M', '104', 'F', '106-116',  
A;Experimental source: cv. Bonminor  
A;Note: parts of the A4 chain, including the amino end, were sequenced  
C;Comment: The source of this protein was cotyledon tissue taken from seeds at the middle  
C;Comment: The glycinin molecule, the major seed storage protein of soybean, is composed  
identified.  
C;Comment: Acidic (A5 and A4) and basic (B3) components of this glycinin subunit are syn-  
sulfide bond, that is thought to be noncovalently associated with the A4 chain.  
C;Superfamily: glycinin  
C;Keywords: seed; storage protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-120/Product: glycinin, A5 chain #status experimental <GA5>  
F;121-377/Product: glycinin, A4 chain #status predicted <GA4>  
F;378-562/Product: glycinin, B3 chain #status predicted <GB3>  
F;108-384/Disulfide bonds: #status predicted

Query Match 89.7%; Score 52; DB 1; Length 562;  
Best Local Similarity 88.9%; Pred. No. 1.1;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPT 9  
|||:||||  
Db 149 IPPSVPT 157

RESULT 9  
JC2097  
legumin type B alpha chain precursor (clone LeB4, B4) - tick bean  
C;Species: Vicia faba var. minor (tick bean)  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 06-Dec-1996  
C;Accession: JC2097  
R;Horstmann, C.; Schlesier, B.; Otto, A.; Kostka, S.; Muentz, K.  
Theor. Appl. Genet. 86, 867-874, 1993  
A;Title: Polymorphism of legumin subunits from field bean (Vicia faba L. var. minor) and  
A;Reference number: JC2094  
A;Accession: JC2097  
A;Molecule type: DNA  
A;Residues: 1-290 <HOR>  
C;Superfamily: glycinin  
C;Keywords: seed; storage protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-268/Product: legumin type B alpha chain #status predicted <MAT>

Query Match 84.5%; Score 49; DB 2; Length 290;  
Best Local Similarity 77.8%; Pred. No. 1.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPT 9  
|||:||||  
Db 147 IPPGIPYT 155

RESULT 10  
A24942  
legumin B4 precursor - fava bean  
C;Species: Vicia faba (fava bean)  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 13-Nov-1998  
C;Accession: A24942  
R;Baumlein, H.; Wobus, U.; Pustell, J.; Kafatos, F.C.  
Nucleic Acids Res. 14, 2707-2720, 1986  
A;Title: The legumin gene family: structure of a B type gene of Vicia faba and a possible  
A;Reference number: A24942; MUID:86176760; PMID:3960730  
A;Accession: A24942  
A;Molecule type: DNA  
A;Residues: 1-484 <BAE>  
A;Note: the authors translated the codon GTT for residue 188 as Gly and CAC for residue  
C;Superfamily: glycinin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-483/Product: legumin B4 #status predicted <MAT>

Query Match 84.5%; Score 49; DB 2; Length 484;  
Best Local Similarity 77.8%; Pred. No. 2.9;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPT 9  
|||:||||  
Db 147 IPPGIPYT 155

RESULT 11  
S44268  
legumin B precursor - spring vetch  
C;Species: Vicia sativa (spring vetch, tare)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S44268  
R;Nong, V.; Becker, C.; Muentz, K.  
submitted to the EMBL Data Library, April 1994  
A;Description: Cloning and heterologous expression of cDNAs encoding legumine of vetch  
A;Reference number: S44266  
A;Accession: S44268  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-485 <NON>  
A;Cross-references: UNIPROT:Q41703; EMBL:Z32796; NID:G479103; PIDN:CAA83674.1; PID:G479  
C;Superfamily: glycinin

Query Match 84.5%; Score 49; DB 2; Length 485;  
Best Local Similarity 77.8%; Pred. No. 2.9;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPT 9  
|||:||||  
Db 152 IPPGIPYT 160

RESULT 12  
S26688  
legumin K - garden pea  
C;Species: Pisum sativum (garden pea)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 12-Apr-1995  
C;Accession: S26688  
R;Thompson, A.J.; Bown, D.; Yaish, S.; Gatehouse, J.A.  
Biochem. Physiol. Pflanz. 187, 1-12, 1991  
A;Title: Differential expression of seed storage protein genes in the pea legJ subfamily  
A;Reference number: S26688  
A;Accession: S26688  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-500 <THO>  
 A;Cross-references: EMBL:X67423  
 C;Genetics:  
 A;Start codon: GTG  
 A;Introns: 183/3; 375/3  
 C;Superfamily: glycinin

Query Match 84.5%; Score 49; DB 2; Length 500;  
 Best Local Similarity 77.8%; Pred. No. 3;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPIYWT 9  
 ||| :|||  
 Db 147 IPSGIPYWT 155

## RESULT 13

S00336  
 legumin B LegJ precursor - garden pea  
 N;Alternate names: minor legumin LegJ  
 C;Species: Pisum sativum (garden pea)  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
 C;Accession: S00336  
 R;Gatehouse, J.A.; Bown, D.; Gilroy, J.; Levasseur, M.; Castleton, J.; Ellis, T.H.N.  
 Biochem. J. 250, 15-24, 1988  
 A;Title: Two genes encoding 'minor' legumin polypeptides in pea (Pisum sativum L.). Char  
 A;Reference number: S00336; MUID:88183306; PMID:3355508  
 A;Accession: S00336  
 A;Molecule type: DNA  
 A;Residues: 1-503 <GAT>  
 A;Cross-references: UNIPROT:P05692; EMBL:X07014; NID:G20782; PIDN:CAA30067.1; PID:G20783  
 A;Note: part of this sequence, including the amino end of both the alpha and beta chains  
 C;Genetics:  
 A;Gene: LegJ  
 A;Introns: 183/3; 378/3  
 C;Superfamily: glycinin  
 F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-322/Product: legumin B alpha chain #status experimental <ACH>  
 F;323-503/Product: legumin B beta chain #status experimental <BCH>

Query Match 84.5%; Score 49; DB 2; Length 503;  
 Best Local Similarity 77.8%; Pred. No. 3.1;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPIYWT 9  
 ||| :|||  
 Db 147 IPSGIPYWT 155

## RESULT 14

FWSYG3  
 Glycinin G5 precursor - soybean  
 N;Alternate names: 11S globulin; glycinin A3B4  
 C;Species: Glycine max (soybean)  
 C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
 C;Accession: A92524; S11005; A05083; A22615  
 R;Fukazawa, C.; Momma, T.; Hirano, H.; Harada, K.; Uda, K.  
 J. Biol. Chem. 260, 6234-6239, 1985  
 A;Title: Glycinin A3B4 mRNA: cloning and sequencing of double-stranded cDNA complementar  
 A;Reference number: A92524; MUID:85207609; PMID:3838983  
 A;Accession: A92524  
 A;Molecule type: mRNA  
 A;Residues: 1-516 <FUK>

A;Cross-references: UNIPROT:P04347; GB:M10962; NID:G169968; PIDN:AAA33964.1; PID:G169969  
 R;Experimental source: cv. Boninori  
 R;Hirano, H.; Fukazawa, C.; Harada, K.  
 J. Biol. Chem. 259, 14371-14377, 1984  
 A;Title: The complete amino acid sequence of the A-3 subunit of the glycinin seed storag  
 A;Reference number: A92465; MUID:85054904; PMID:6542104  
 A;Contents: annotation  
 A;Note: the sequence reported is very different from that shown  
 R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallion, B.J.; Fischer, R.L.;  
 Plant Cell 1, 313-328, 1989

A;Title: Characterization of the glycinin gene family in soybean.  
 A;Reference number: S10851; MUID:92393391; PMID:2485233  
 A;Accession: S11005  
 A;Molecule type: DNA  
 A;Residues: 1-516 <NIE>  
 A;Experimental source: variety Forrest  
 C;Genetics:  
 A;Gene: GY5  
 C;Superfamily: glycinin  
 C;Keywords: seed; storage protein  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-344/Product: glycinin chain A3 #status predicted <GLA>  
 F;345-516/Product: glycinin chain B4 #status predicted <GLB>  
 F;109-351/Disulfide bonds: #status predicted

Query Match 82.8%; Score 48; DB 1; Length 516;  
 Best Local Similarity 88.9%; Pred. No. 4.5;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IPPGVPIYWT 9  
 ||| :|||  
 Db 149 IPLGVPIYWT 157

## RESULT 15

T40893  
 Hypothetical protein SPC1259.04 - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T40893  
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Boche, G.; Pohl, T.  
 submitted to the EMBL Data Library, December 1998  
 A;Reference number: Z21955  
 A;Accession: T40893  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-168 <WOO>  
 A;Cross-references: UNIPROT:O94704; EMBL:AL034564; PIDN:CAA22542.1; GSPDB:GN00068; SPDB:  
 A;Experimental source: strain 972h-; cosmid c1259  
 C;Genetics:  
 A;Gene: SPDB:SPCC1259.04  
 A;Map position: 3  
 A;Introns: 47/2

Query Match 74.1%; Score 43; DB 2; Length 168;  
 Best Local Similarity 85.7%; Pred. No. 8.7;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPGVPYWT 8  
 ||| :|||  
 Db 68 PPGSPYWT 74

Search completed: November 6, 2004, 19:54:15  
 Job time : 23.9375 secs